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#12

1638

RAW SEQUENCE LISTING DATE: 06/05/2000
 PATENT APPLICATION: US/09/142,108A TIME: 11:41:24

Input Set : A:\PTO.txt
 Output Set: N:\CRF3\06022000\I142108A.raw

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4 <110> APPLICANT: International Flower Developments Pty Ltd
 6 <120> TITLE OF INVENTION: Genetic sequences encoding flavonoid pathway enzymes
 7 and uses therefor
 9 <130> FILE REFERENCE: 2088133
 11 <140> CURRENT APPLICATION NUMBER: 09/142108A
 C--> 12 <141> CURRENT FILING DATE: 1999-03-29
 14 <150> PRIOR APPLICATION NUMBER: PN8386
 15 <151> PRIOR FILING DATE: 1996-03-01
 17 <160> NUMBER OF SEQ ID NOS: 41
 19 <170> SOFTWARE: PatentIn Ver. 2.1
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 1789
 23 <212> TYPE: DNA
 24 <213> ORGANISM: Petunia x hybrida
 26 <220> FEATURE:
 27 <221> NAME/KEY: CDS
 28 <222> LOCATION: (50)..(1588)
 30 <400> SEQUENCE: 1
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 32 Met Glu Ile
 33 1
 35 tta agc cta att ctg tac acc gtc att ttc tca ttt ctt cta caa ttc 106
 36 Leu Ser Leu Ile Leu Tyr Thr Val Ile Phe Ser Phe Leu Leu Gln Phe
 37 5 10 15
 39 att ctt aga tca ttt ttc cgt aaa cgt tac cct tta cca tta cca cca 154
 40 Ile Leu Arg Ser Phe Phe Arg Lys Arg Tyr Pro Leu Pro Leu Pro Pro
 41 20 25 30 35
 43 ggt cca aaa cca tgg cca att ata gga aac cta gtc cat ctt gga ccc 202
 44 Gly Pro Lys Pro Trp Pro Ile Ile Gly Asn Leu Val His Leu Gly Pro
 45 40 45 50
 47 aaa cca cat caa tca act gca gcc atg gct caa act tat gga cca ctc 250
 48 Lys Pro His Gln Ser Thr Ala Ala Met Ala Gln Thr Tyr Gly Pro Leu
 49 55 60 65
 51 atg tat ctt aag atg ggg ttc gta gac gtg gtg gtt gca gcc tcg gca 298
 52 Met Tyr Leu Lys Met Gly Phe Val Asp Val Val Val Ala Ala Ser Ala
 53 70 75 80
 55 tcg gtt gca gct cag ttc ttg aaa act cat gat gct aat ttc tcg agc 346
 56 Ser Val Ala Ala Gln Phe Leu Lys Thr His Asp Ala Asn Phe Ser Ser
 57 85 90 95
 59 cgt cca cca aat tct ggt gca gaa cat atg gct tat aat tat cag gat 394
 60 Arg Pro Pro Asn Ser Gly Ala Glu His Met Ala Tyr Asn Tyr Gln Asp
 61 100 105 110 115
 63 ctt gtt ttt gca cct tat gga cct aga tgg cgt atg ctt agg aaa att 442
 64 Leu Val Phe Ala Pro Tyr Gly Pro Arg Trp Arg Met Leu Arg Lys Ile
 65 120 125 130
 67 tgc tca gtt cac ctt ttc tct acc aag gct tta gat gac ttc cgc cat 490
 68 Cys Ser Val His Leu Phe Ser Thr Lys Ala Leu Asp Asp Phe Arg His

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69          135          140          145
71 gtc cgc cag gat gaa gtg aaa aca ctg acg cgc gca cta gca agt gca 538
72 Val Arg Gln Asp Glu Val Lys Thr Leu Thr Arg Ala Leu Ala Ser Ala
73          150          155          160
75 ggc caa aag cca gtc aaa tta atg ggt cag tta ttg aac gtg tgc acg acg 586
76 Gly Gln Lys Pro Val Lys Leu Gly Gln Leu Leu Asn Val Cys Thr Thr
77          165          170          175
79 aac gca ctc gcg cga gta atg cta ggt aag cga gta ttt gcc gac gga 634
80 Asn Ala Leu Ala Arg Val Met Leu Gly Lys Arg Val Phe Ala Asp Gly
81 180          185          190          195
83 agt ggc gat gtt gat cca caa gcg gcg gag ttc aag tca atg gtg gtg 682
84 Ser Gly Asp Val Asp Pro Gln Ala Ala Glu Phe Lys Ser Met Val Val
85          200          205          210
87 gaa atg atg gta gtc gcc ggt gtt ttt aac att ggt gat ttt att ccg 730
88 Glu Met Met Val Val Ala Gly Val Phe Asn Ile Gly Asp Phe Ile Pro
89          215          220          225
91 caa ctt aat tgg tta gat att caa ggt gta gcc gct aaa atg aag aag 778
92 Gln Leu Asn Trp Leu Asp Ile Gln Gly Val Ala Ala Lys Met Lys Lys
93          230          235          240
95 ctc cac gcg cgt ttc gac gcg ttc ttg act gat ata ctt gaa gag cat 826
96 Leu His Ala Arg Phe Asp Ala Phe Leu Thr Asp Ile Leu Glu Glu His
97          245          250          255
99 aag ggt aaa att ttt gga gaa atg aaa gat ttg ttg agt act ttg atc 874
100 Lys Gly Lys Ile Phe Gly Glu Met Lys Asp Leu Leu Ser Thr Leu Ile
101 260          265          270          275
103 tct ctt aaa aat gat gat gcg gat aat gat gga ggg aaa ctc act gat 922
104 Ser Leu Lys Asn Asp Asp Ala Asp Asn Asp Gly Gly Lys Leu Thr Asp
105          280          285          290
107 aca gaa att aaa gca tta ctt ttg aac ttg ttt gta gct gga aca gac 970
108 Thr Glu Ile Lys Ala Leu Leu Leu Asn Leu Phe Val Ala Gly Thr Asp
109          295          300          305
111 aca tct tct agt aca gtt gaa tgg gcc att gct gag ctt att cgt aat 1018
112 Thr Ser Ser Ser Thr Val Glu Trp Ala Ile Ala Glu Leu Ile Arg Asn
113          310          315          320
115 cca aaa ata cta gcc caa gcc cag caa gag atc gac aaa gtc gtt gga 1066
116 Pro Lys Ile Leu Ala Gln Ala Gln Gln Glu Ile Asp Lys Val Val Gly
117          325          330          335
119 agg gac cgg cta gtt ggc gaa ttg gac cta gcc caa ttg aca tac ttg 1114
120 Arg Asp Arg Leu Val Gly Glu Leu Asp Leu Ala Gln Leu Thr Tyr Leu
121 340          345          350          355
123 gaa gct ata gtc aag gaa acc ttt cgg ctt cat cca tca acc cct ctt 1162
124 Glu Ala Ile Val Lys Glu Thr Phe Arg Leu His Pro Ser Thr Pro Leu
125          360          365          370
127 tca ctt cct aga att gca tct gag agt tgt gag atc aat ggc tat ttc 1210
128 Ser Leu Pro Arg Ile Ala Ser Glu Ser Cys Glu Ile Asn Gly Tyr Phe
129          375          380          385
131 att cca aaa ggc tca acg ctt ctc ctt aat gtt tgg gcc att gct cgt 1258
132 Ile Pro Lys Gly Ser Thr Leu Leu Leu Asn Val Trp Ala Ile Ala Arg
133          390          395          400

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135 gat cca aat gca tgg gct gat cca ttg gag ttt agg cct gaa agg ttt 1306
136 Asp Pro Asn Ala Trp Ala Asp Pro Leu Glu Phe Arg Pro Glu Arg Phe
137 405 410 415
139 ttg cca gga ggt gag aag ccc aaa gtt gat gtc cgt ggg aat gac ttt 1354
140 Leu Pro Gly Gly Glu Lys Pro Lys Val Asp Val Arg Gly Asn Asp Phe
141 420 425 430 435
143 gaa gtc ata cca ttt gga gct gga cgt agg att tgt gct gga atg aat 1402
144 Glu Val Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala Gly Met Asn
145 440 445 450
147 ttg ggt ata cgt atg gtc cag ttg atg att gca act tta ata cat gca 1450
148 Leu Gly Ile Arg Met Val Gln Leu Met Ile Ala Thr Leu Ile His Ala
149 455 460 465
151 ttt aac tgg gat ttg gtc agt gga caa ttg ccg gag atg ttg aat atg 1498
152 Phe Asn Trp Asp Leu Val Ser Gly Gln Leu Pro Glu Met Leu Asn Met
153 470 475 480
155 gaa gaa gca tat ggg ctg acc tta caa cgg gct gat cca ttg gtt gtg 1546
156 Glu Glu Ala Tyr Gly Thr Leu Gln Arg Ala Asp Pro Leu Val Val
157 485 490 495
159 cac cca agg cct cgc tta gaa gcc caa gcg tac att ggg tga 1588
160 His Pro Arg Pro Arg Leu Glu Ala Gln Ala Tyr Ile Gly
161 500 505 510
163 gcagcaacag cccatggaga taacatgagt gttaaatgta tgagtcctcca tatcttgttt 1648
165 agttttgttta tgctttggat ttagtagttt ttatatgtat agatcaatgt ttgcattgtc 1708
167 agtaagaata tccgttgctt gtttcattaa ctccagggtgg acaataaaaag aagtaatttg 1768
169 tatgaaaaaa aaaaaaaaaa a 1789
172 <210> SEQ ID NO: 2
173 <211> LENGTH: 512
174 <212> TYPE: PRT
175 <213> ORGANISM: Petunia x hybrida
177 <400> SEQUENCE: 2
178 Met Glu Ile Leu Ser Leu Ile Leu Tyr Thr Val Ile Phe Ser Phe Leu
179 1 5 10 15
180 Leu Gln Phe Ile Leu Arg Ser Phe Phe Arg Lys Arg Tyr Pro Leu Pro
181 20 25 30
182 Leu Pro Pro Gly Pro Lys Pro Trp Pro Ile Ile Gly Asn Leu Val His
183 35 40 45
184 Leu Gly Pro Lys Pro His Gln Ser Thr Ala Ala Met Ala Gln Thr Tyr
185 50 55 60
186 Gly Pro Leu Met Tyr Leu Lys Met Gly Phe Val Asp Val Val Val Ala
187 65 70 75 80
188 Ala Ser Ala Ser Val Ala Ala Gln Phe Leu Lys Thr His Asp Ala Asn
189 85 90 95
190 Phe Ser Ser Arg Pro Pro Asn Ser Gly Ala Glu His Met Ala Tyr Asn
191 100 105 110
192 Tyr Gln Asp Leu Val Phe Ala Pro Tyr Gly Pro Arg Trp Arg Met Leu
193 115 120 125
194 Arg Lys Ile Cys Ser Val His Leu Phe Ser Thr Lys Ala Leu Asp Asp
195 130 135 140
196 Phe Arg His Val Arg Gln Asp Glu Val Lys Thr Leu Thr Arg Ala Leu

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RAW SEQUENCE LISTING

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TIME: 11:41:25

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Output Set: N:\CRF3\06022000\I142108A.raw

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197 145          150          155          160
198 Ala Ser Ala Gly Gln Lys Pro Val Lys Leu Gly Gln Leu Leu Asn Val
199          165          170          175
200 Cys Thr Thr Asn Ala Leu Ala Arg Val Met Leu Gly Lys Arg Val Phe
201          180          185          190
202 Ala Asp Gly Ser Gly Asp Val Asp Pro Gln Ala Ala Glu Phe Lys Ser
203          195          200          205
204 Met Val Val Glu Met Met Val Val Ala Gly Val Phe Asn Ile Gly Asp
205          210          215          220
206 Phe Ile Pro Gln Leu Asn Trp Leu Asp Ile Gln Gly Val Ala Ala Lys
207 225          230          235          240
208 Met Lys Lys Leu His Ala Arg Phe Asp Ala Phe Leu Thr Asp Ile Leu
209          245          250          255
210 Glu Glu His Lys Gly Lys Ile Phe Gly Glu Met Lys Asp Leu Leu Ser
211          260          265          270
212 Thr Leu Ile Ser Leu Lys Asn Asp Asp Ala Asp Asn Asp Gly Gly Lys
213          275          280          285
214 Leu Thr Asp Thr Glu Ile Lys Ala Leu Leu Leu Asn Leu Phe Val Ala
215          290          295          300
216 Gly Thr Asp Thr Ser Ser Thr Val Glu Trp Ala Ile Ala Glu Leu
217 305          310          315          320
218 Ile Arg Asn Pro Lys Ile Leu Ala Gln Ala Gln Gln Glu Ile Asp Lys
219          325          330          335
220 Val Val Gly Arg Asp Arg Leu Val Gly Glu Leu Asp Leu Ala Gln Leu
221          340          345          350
222 Thr Tyr Leu Glu Ala Ile Val Lys Glu Thr Phe Arg Leu His Pro Ser
223          355          360          365
224 Thr Pro Leu Ser Leu Pro Arg Ile Ala Ser Glu Ser Cys Glu Ile Asn
225          370          375          380
226 Gly Tyr Phe Ile Pro Lys Gly Ser Thr Leu Leu Leu Asn Val Trp Ala
227 385          390          395          400
228 Ile Ala Arg Asp Pro Asn Ala Trp Ala Asp Pro Leu Glu Phe Arg Pro
229          405          410          415
230 Glu Arg Phe Leu Pro Gly Gly Glu Lys Pro Lys Val Asp Val Arg Gly
231          420          425          430
232 Asn Asp Phe Glu Val Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala
233          435          440          445
234 Gly Met Asn Leu Gly Ile Arg Met Val Gln Leu Met Ile Ala Thr Leu
235          450          455          460
236 Ile His Ala Phe Asn Trp Asp Leu Val Ser Gly Gln Leu Pro Glu Met
237 465          470          475          480
238 Leu Asn Met Glu Glu Ala Tyr Gly Leu Thr Leu Gln Arg Ala Asp Pro
239          485          490          495
240 Leu Val Val His Pro Arg Pro Arg Leu Glu Ala Gln Ala Tyr Ile Gly
241          500          505          510
245 <210> SEQ ID NO: 3
246 <211> LENGTH: 1745
247 <212> TYPE: DNA
248 <213> ORGANISM: Dianthus caryophyllus

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VERIFICATION SUMMARY

DATE: 06/05/2000

PATENT APPLICATION: US/09/142,108A

TIME: 11:41:26

Input Set : A:\PTO.txt

Output Set: N:\CRF3\06022000\I142108A.raw

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:955 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:959 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:963 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:967 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:971 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:975 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:979 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:983 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:987 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:991 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:995 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:999 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:1003 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:1007 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:1011 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:1015 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:1019 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:1023 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:1027 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:1031 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:1035 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:1039 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:1043 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:1047 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:1051 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:1054 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#: 9, CDS LOCATION:3421..3907
L:1055 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:2833 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:32
L:2838 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:32
L:2843 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:32
L:2848 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:32
L:2853 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32
L:2878 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:34
L:2883 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:34
L:2888 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:34
L:2893 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34
L:2905 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:35
L:2910 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:35
L:2915 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:35
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L:2931 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:35
L:2936 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:35
L:2941 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:35
L:2946 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35
L:2957 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:36
L:2957 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:36

VERIFICATION SUMMARY

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TIME: 11:41:26

Input Set : A:\PTO.txt

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L:2957 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:36
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L:2974 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:37
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L:2984 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:37
L:2989 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:37
L:2994 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:37
L:2999 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:37
L:3004 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37
L:3048 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:41
L:3053 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:41
L:3058 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:41
L:3063 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:41
L:3068 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:41
L:3073 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:41
L:3078 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:41
L:3083 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41



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